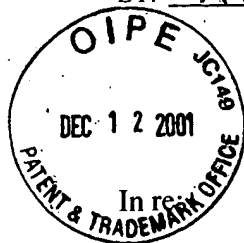


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BY: Helene Gabel

DATE: October 24, 2001

PATENT



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent Application
of Ian Hector Frazer *et al.*

Conf. No.: 4929

Appln. No.: 09/900,345 /

Filed: July 6, 2001

For: METHOD AND POLYNUCLEOTIDES : Attorney Docket
FOR DETERMINING TRANSLATIONAL : No. 10338-5 US
EFFICIENCY OF A CODON : (2423066/VPA)

**CLAIM OF FOREIGN PRIORITY AND
TRANSMITTAL OF PRIORITY DOCUMENT**

Applicants hereby confirm their claim of the right of foreign priority under 35 U.S.C. Section 119 for the above-identified patent application. The claim of foreign priority is based upon Application No. PP 8078, filed in Australia on January 8, 1999, and International Application No. PCT/AU00/00008, filed in Australia on January 7, 2000, and the benefit of those dates is claimed.

Submitted herewith are certified copies of both Australian Applications identified in the paragraph above. It is submitted that these documents complete the requirements of 35 U.S.C. Section 119, and benefit of the foreign priority is respectfully requested.

Respectfully submitted,

IAN HECTOR FRAZER *ET AL.*

Oct. 24, 2001
(Date)

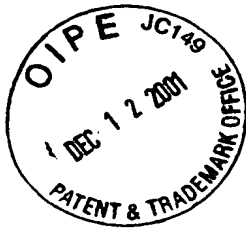
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**Patent Office
Canberra**

I, GAYE TURNER, TEAM LEADER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. PP 8078 for a patent by THE UNIVERSITY OF QUEENSLAND filed on 08 January 1999.

WITNESS my hand this
Fifth day of October 2001

GAYE TURNER
TEAM LEADER EXAMINATION
SUPPORT AND SALES

AUSTRALIA

Patents Act 1990

PROVISIONAL SPECIFICATION

Invention Title: "CODON UTILIZATION"

The invention is described in the following statement:

TITLE"CODON UTILIZATION"

5

FIELD OF THE INVENTION

THIS INVENTION relates generally to gene expression and in particular, a method and polynucleotides for determining codon utilization in one or more cells or tissues of an organism. More particularly, the method and polynucleotides of the invention are concerned with ascertaining codon preferences in cells or tissues for purposes of modifying the translational efficiency of protein-encoding polynucleotides in those cells or tissues.

BACKGROUND OF THE INVENTION

It is well known that a "triplet" codon of four possible nucleotide bases can exist in 64 variant forms. These forms provide the message for only 20 different amino acids (as well as translation initiation and termination) and this means that some amino acids can be encoded by more than one codon. In this context, some amino acids have as many as six "redundant", alternative codons while some others have a single, required codon.

For reasons not completely understood, codon utilization is highly biased in that alternative codons are not at all uniformly present in the endogenous DNA of differing cell types. In this regard, there appears to exist a variable natural hierarchy of "preference" for certain codons between different cell types or between different organisms.

Codon usage patterns have been shown to correlate with relative abundance of isoaccepting transfer RNA (iso-tRNA) species, and with genes encoding proteins of high versus low abundance. Moreover, the present inventors recently discovered that the intracellular abundance of different iso-tRNAs varies in different cells or tissues of a single multi-cellular organism (see copending International Application No. PCT/AU98/00530).

The implications of codon preference phenomena on gene expression are manifest in that these phenomena can affect the translational efficiency of messenger RNA (mRNA). In this regard, it is widely known that translation of "rare codons", for which the corresponding iso-tRNA is in relatively low abundance, may cause a ribosome to pause during translation which can lead to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation.

A primary goal in recombinant research is to provide transgenic organisms which express a foreign gene in an amount sufficient to confer the desired phenotype to the organism. However, expression of the foreign gene may be severely impeded if a particular host cell of the organism or the organism itself has a low abundance of iso-tRNAs corresponding to one or more codons of the foreign gene. Accordingly, a major aim of investigators in this field is to first ascertain the codon preference for particular cells or tissues in which a foreign gene is to be expressed, and subsequently alter the codon composition of the foreign gene for optimized expression in those cells or tissues.

Codon preference may be determined simply by analyzing the frequency at which codons are used by genes expressed by a particular cell or tissue or by a

plurality of cells or tissues of a given organism. Codon frequency tables as well as suitable methods for determining frequency of codon usage in an organism are described, for example, in an article by Sharp et al (1988, *Nucleic Acids Res.* 16 8207-8211). The relative level of gene expression (e.g., detectable protein expression versus no detectable protein expression) can provide an indirect measure of the relative abundance of specific iso-tRNAs expressed in different cells or tissues.

Alternatively, codon preference may be determined by measuring the relative intracellular abundance of different iso-tRNA species. For example, reference may be made to copending International Application No. PCT/AU98/00530 which describes a method that utilizes labeled oligonucleotides specific for different iso-tRNAs to probe an RNA extract prepared from a particular cell or tissue type.

The above methods provide useful indirect evidence for determining codon preference. However, such indirect evidence may not provide an accurate indication of the translational efficiency of a given codon. Accordingly, there is a need to provide a method which more directly ascertains the translational efficiency of a codon in a cell or tissue.

OBJECT OF THE INVENTION

It is therefore an object of the present invention to provide a method for determining codon preference in cells or tissues which method ameliorates at least some of the disadvantages associated with the prior art.

SUMMARY OF THE INVENTION

Accordingly, in one aspect of the invention, there is provided a method for determining relative preference for a codon in at least one cell or tissue type, said method including the steps of:-

(A) introducing into said at least one cell or tissue type a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of identical codons corresponding to said codon under test, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory nucleotide sequences;

(B) expressing said synthetic construct in said at least one cell or tissue type; and

(C) measuring activity associated with said reporter protein in said at least one cell or tissue type to thereby determine the relative preference for said codon.

Preferably, the method is further characterized by the steps of:-

(i) introducing into another of said at least one cell or tissue type a different synthetic construct having said reporter polynucleotide fused in frame with a tandem repeat of identical codons corresponding to a different codon under test, wherein said different codon is synonymous with said first-mentioned codon, and wherein said different synthetic construct is operably linked to one or more regulatory nucleotide sequences;

(ii) expressing said different synthetic construct in said another of said at least one cell or tissue type;

(iii) measuring activity associated with said reporter protein in said another of said at least one cell or tissue type; and

5 (iv) comparing the respective activities associated with said reporter protein from said synthetic constructs to thereby determine the preference for said first-mentioned codon relative to the preference for said different codon.

10 Preferably, step (A) of the above method is further characterized by the steps of:-

(a) introducing the synthetic construct into a progenitor cell or tissue of said at least one cell or tissue type; and

15 (b) generating said at least one cell or tissue type from said progenitor cell or tissue;

wherein said at least one cell or tissue type contains said synthetic construct.

Suitably, the method is further characterized by the steps of:-

20 (1) introducing the synthetic construct into a progenitor cell or tissue of said at least one cell or tissue type; and

(2) growing an organism or part thereof from said progenitor cell or tissue;

25 wherein said organism comprises said at least one cell or tissue type containing said synthetic construct.

30 The method may be further characterized by the step of introducing the synthetic construct into an organism or part thereof such that said synthetic construct is introduced into said at least one cell or tissue type.

35 In another aspect, the invention resides in a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of identical codons, wherein said reporter polynucleotide

encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory nucleotide sequences

5

DETAILED DESCRIPTION

By "expressing said synthetic construct" is meant transcribing the synthetic construct such that mRNA is produced.

10

The term "synonymous codon" as used herein refers to a codon having a different nucleotide sequence to an existing codon but encoding the same amino acid as the existing codon.

15

By "isoaccepting transfer RNA" or "iso-tRNA" is meant one or more transfer RNA molecules that differ in their anticodon structure but are specific for the same amino acid.

The term "polynucleotide" as used herein designates mRNA, RNA, cRNA, cDNA or DNA.

20

The term "progenitor cell or tissue" as used herein refers to a cell or tissue that can give rise to a particular cell or tissue in which codon preference is to be determined.

25

Throughout this specification, unless the context requires otherwise, the words "comprise", "comprises" and "comprising" will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

30

The present invention is based on the discovery that different stretches of identical codons fused respectively in frame with a reporter polynucleotide can give rise to different levels of reporter protein expressed within a given cell type.

35

Not wishing to be bound by theory, it is believed that a tandem series of identical codons may cause a

ribosome to pause during translation if the iso-tRNA corresponding to the identical codons is limiting. In this regard, it is well known that ribosomal pausing leads to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation. Accordingly, the levels of reporter protein expressed in the different cells or tissues will be sensitive to the intracellular abundance of the iso-tRNA species corresponding to the identical codons and will therefore provide a direct correlation a cell's or tissue's preference for a given codon. This means for example, that if the levels of the reporter protein obtained in a cell or tissue type are lower with a synthetic construct having a tandem series of identical first codons compared to those expressed in the same cell or tissue type with a different synthetic construct having a tandem series of identical second codons, wherein the first codons are different to, but synonymous with, the second codons, then it can be deduced that the cell or tissue has a higher preference for the second codon relative to the first codon with respect to translation.

Suitably, the tandem repeat comprises at least three identical codons. Preferably, the tandem repeat comprises four identical codons, more preferably five, six, or seven identical codons. However, it will be appreciated that the number of identical codons utilized for the synthetic construct may vary depending, for example, on the regulatory sequences used to express the synthetic construct, the reporter polynucleotide employed, and the cell or tissue under test. Accordingly, it is preferred that preliminary experiments be carried out to determine an optimal number of identical codons which is sensitive to the intracellular abundance of the corresponding iso-tRNA species, when expressed as part of the

synthetic construct. In this regard, too many identical codons may completely inhibit expression of the reporter protein whilst too few may not influence reporter protein expression at all.

5 The tandem repeat may be fused at a location adjacent to, or within, the reporter polynucleotide. The location is preferably selected such that the tandem repeat interferes with translation of at least a portion of the reporter protein from which an
10 activity can be measured. Preferably, the tandem repeat is located immediately upstream of the reporter polynucleotide.

 The reporter polynucleotide may encode any suitable protein whose levels may be determined
15 directly, or indirectly such as by suitable assay. Suitable reporter polynucleotides include, but are not restricted to, polynucleotides encoding β -galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyltransferase (CAT),
20 β -glucuronidase (GUS), herbicide resistance genes such as the bialophos resistance (BAR) gene that confers resistance to the herbicide BASTA, and green fluorescent protein (GFP). Assays for the activities associated with such proteins are well known by those
25 of skill in the art. Preferably, the reporter polynucleotide encodes GFP.

 Of course it will be appreciated that reporter polynucleotides need not correspond to a full-length gene encoding a particular reporter
30 protein. Accordingly, the invention also contemplates reporter polynucleotide sub-sequences encoding desired portions of the reporter protein. A polynucleotide sub-sequence encodes a domain of the reporter protein having an activity associated
35 therewith and preferably encodes at least 10, 20, 50,

100, 150, or 500 contiguous amino acids of the reporter protein.

5 The method of the invention is applicable to any suitable cell or tissue type. For example, the cell or tissue type may be of mammalian or plant origin. The cell or tissue type may be of any suitable lineage. Suitable cell lines may include, for example, CV-1 cells, COS cells, yeast or spodoptera cells which are capable of being grown in
10 vitro. The invention also contemplates cells which may be prokaryotic in origin.

Suitable methods for isolating particular cells or tissues are well known to those of skill in the art. For example, one can take advantage of one
15 or more particular characteristics of a cell or tissue to specifically isolate the cell or tissue from a heterogeneous population. Such characteristics include, but are not limited to, anatomical location of a tissue, cell density, cell size, cell morphology, cellular metabolic activity, cell uptake of ions such
20 as Ca^{2+} , K^+ , and H^+ ions, cell uptake of compounds such as stains, markers expressed on the cell surface, protein fluorescence, and membrane potential. Suitable methods that may be used in this regard
25 include surgical removal of tissue, flow cytometry techniques such as fluorescence-activated cell sorting (FACS), immunoaffinity separation (e.g., magnetic bead separation such as Dynabead™ separation), density separation (e.g., metrizamide, Percoll™, or Ficoll™
30 gradient centrifugation), and cell-type specific density separation.

In an alternate embodiment, progenitor cells or tissues may be used for initially introducing the synthetic construct. Any suitable progenitor cell or
35 tissue may be used which gives rise to a particular

cell or tissue of interest for which codon preference is to be ascertained. For example, a suitable progenitor cell may comprise an undifferentiated cell. In the case of a plant, a suitable progenitor cell may include, for example, a meristematic cell whereas a progenitor tissue may include, for example, a callus tissue.

In another embodiment, the synthetic construct may be introduced firstly into an organism or part thereof before subsequent expression of the construct in a particular cell or tissue type. Any suitable organism is contemplated by the invention which may include unicellular as well as multi-cellular organisms. Exemplary multi-cellular organisms include mammals and plants.

The construction of the synthetic construct may be effected by any suitable technique. For example, *in vitro* mutagenesis methods may be employed which are well known to those of skill in the art. Suitable mutagenesis methods are described for example in the relevant sections of CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (Ausubel, et al., eds.) (John Wiley & Sons, Inc. 1997), and of MOLECULAR CLONING. A LABORATORY MANUAL (Sambrook, et al., eds.) (Cold Spring Harbor Press, 1989), which are incorporated herein by reference. Alternatively, suitable methods for altering DNA are set forth, for example, in U.S. Patent Nos. 4,184,917, 4,321,365 and 4,351,901, which are incorporated herein by reference. Instead of *in vitro* mutagenesis, the synthetic polynucleotide may be synthesized *de novo* using readily available machinery. Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652, which is incorporated herein by reference. However, it should be noted that the present invention is not dependent on and not

directed to any one particular technique for constructing the synthetic construct.

Regulatory nucleotide sequences which may be utilized to regulate expression of the synthetic polynucleotide include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory sequences are well known to those of skill in the art. Suitable promoters which may be utilized to induce expression of the polynucleotides of the invention include constitutive promoters and inducible promoters.

Synthetic constructs according to the invention may be operably linked to one or more regulatory sequences in the form of an expression vector. By "vector" is meant a nucleic acid molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, or plant virus, into which a synthetic nucleic acid sequence may be inserted or cloned. A vector preferably contains one or more unique restriction sites and may be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integratable with the genome of the defined host such that the cloned sequence is reproducible. Thus, by "expression vector" is meant any autonomous element capable of directing the synthesis of a protein. Such expression vectors are well known by practitioners in the art.

The vector may also include a selection marker such as an antibiotic resistance gene which can be used for selection of suitable transformants/transfectants. Examples of such resistance genes include the *nptII* gene which confers resistance to the antibiotics kanamycin and G418

(Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

5 The step of introducing the synthetic construct into a particular cell or tissue type, or into a progenitor cell or tissue thereof, or into an organism or part thereof for subsequent introduction into a particular cell or tissue, will differ depending on the intended use and or species, and may involve lipofection, electroporation, micro-projectile bombardment infection by *Agrobacterium tumefaciens* or 10 *A. rhizogenes*, or protoplast fusion. Such methods are well known to those skilled in the art.

Alternatively, the step of introduction may involve non-viral and viral vectors, cationic 15 liposomes, retroviruses and adenoviruses such as, for example, described in Mulligan, R.C., (1993 *Science* 260 926-932) which is incorporated herein by reference. Such methods may include:

(i) Local application of the synthetic 20 nucleic acid sequence by injection (Wolff et al., 1990, *Science* 247 1465-1468, which is incorporated herein by reference), surgical implantation, instillation or any other means. This method may also be used in combination with local application by 25 injection, surgical implantation, instillation or any other means, of cells responsive to the reporter protein encoded by the synthetic construct. This method may also be used in combination with local application by injection, surgical implantation, 30 instillation or any other means, of another factor or factors required for the activity of said reporter protein.

(ii) General systemic delivery by injection of DNA, (Calabretta et al., 1993, *Cancer Treat. Rev.* 19 169-179, which is incorporated herein 35

by reference), or RNA, alone or in combination with liposomes (Zhu et al., 1993, *Science* 261 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling et al., 1991, *Biotech. Appl. Biochem.* 13 390-405, which is incorporated herein by reference) or any other mediator of delivery. Improved targeting might be achieved by linking the synthetic construct to a targeting molecule (the so-called "magic bullet" approach employing for example, an antibody), or by local application by injection, surgical implantation or any other means, of another factor or factors required for the activity of the protein produced from said synthetic construct, or of cells responsive to said reporter protein.

(iii) Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen et al., 1987, *Mole. Cell Biochem.* 7 2745-2752, or of cationic lipids and polyamines: Rose et al., 1991, *BioTech.* 10 520-525, which articles are incorporated herein by reference), infection, injection, electroporation (Shigekawa et al., 1988, *BioTech.* 6 742-751, which is incorporated herein by reference) or any other way so as to increase the expression of said synthetic construct in those cells. The modification may be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* 260 926-932; Miller, 1992, *Nature* 357 455-460; Salmons et al., 1993, *Hum. Gen. Ther.* 4 129-141, which articles are incorporated herein by reference) or other vectors, or other agents of modification such as liposomes (Zhu et al., 1993, *Science* 261 209-212, which is incorporated herein by reference), viral

capsids or nanoparticles (Bertling et al., 1991, *Biotech. Appl. Biochem.* 13 390-405, which is incorporated herein by reference), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr et al., 1991, *Science* 254 1507-1512 and by Dhawan et al., 1991, *Science* 254 1509-1512, which articles are incorporated herein by reference. Treated cells may be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Advantageously, the relative preference for different codons may be determined by comparing the respective activities of the reporter protein in a given cell or tissue type. One of ordinary skill in the art will thereby be able to determine a relative codon preference table for the cell or tissue type.

The invention further contemplates cells or tissues containing therein the synthetic construct of the invention, or alternatively, cells or tissues produced from the method of the invention.

The invention is further described with reference to the following non-limiting examples.

25 EXAMPLE 1

Construction of expression vectors for determining relative codon preferences in mammalian cells.

Synthetic *gfp* genes will be constructed in which a single artificial start codon (ATG) followed by a stretch of five identical codons is fused in frame immediately upstream of a *gfp* coding sequence. A reverse oligonucleotide primer (SEQ ID NO:180; sequence complementary to the termination codon for GFP, is underlined), and a suite of forward

oligonucleotide primers (SEQ ID NO: 121 through 179; the first codon of GFP, is underlined) will be synthesized and used for PCR amplification of a humanized *gfp* gene (SEQ ID NO:119) (GIBCO) as template with *Taq* DNA polymerase (Amplification parameters: 95°C/30 sec; 52°C/30 sec; 72°C/1 min; 30 cycles). The amplified fragments will have nucleic acid sequences and deduced amino acid sequences as shown in SEQ ID NO:1 through 120. In summary, the synthetic fragments contain an artificial start codon followed by a tandem repeat of five identical codons specific for a given iso-tRNA species. The tandem repeat immediately precedes the second codon of the *gfp* gene. The synthetic fragments by SEQ ID NO and encoded tandem repeat are presented in the TABLE 1.

TABLE 1. Synthetic fragments and tandem repeats encoded thereby.

SEQ ID NO	Tandem repeat	SEQ ID NO	Tandem repeat
1	Ala (GCA) x 5	61	Leu (CTC) x 5
3	Ala (GCC) x 5	63	Leu (CTG) x 5
5	Ala (GCG) x 5	65	Leu (CTT) x 5
7,	Ala (GCT) x 5	67	Leu (TTA) x 5
9	Arg (AGA) x 5	69	Leu (TTG) x 5
11	Arg (AGG) x 5	71	Lys (AAA) x 5
13	Arg (CGA) x 5	73	Lys (AAG) x 5
15	Arg (CGC) x 5	75	Phe (CTT) x 5
17	Arg (CGG) x 5	77	Phe (TTC) x 5
19	Arg (CGT) x 5	79	Pro (CCC) x 5
21	Asn (AAC) x 5	81	Pro (CCG) x 5
23	Asn (AAT) x 5	83	Pro (CCT) x 5
25	Asp (GAC) x 5	85	Pro (CGA) x 5
27	Asp (GAT) x 5	87	Ser (AGC) x 5
29	Cys (TGC) x 5	89	Ser (AGT) x 5

31	Cys (TGT) x 5	91	Ser (TCA) x 5
33	Gln (CAA) x 5	93	Ser (TCC) x 5
35	Gln (CAG) x 5	95	Ser (TCG) x 5
37	Gly (GAA) x 5	97	Ser (TCT) x 5
39	Glu (GAG) x 5	99	Thr (ACA) x 5
41	Gly (GGA) x 5	101	Thr (ACC) x 5
43	Gly (GGC) x 5	103	Thr (ACG) x 5
45	Gly (GGG) x 5	105	Thr (ACT) x 5
47	Gly (GGT) x 5	107	Trp (TGG) x 5
49	His (CAC) x 5	109	Tyr (TAT) x 5
51	His (CAT) x 5	111	Val (GTA) x 5
53	Ile (ATA) x 5	113	Val (GTC) x 5
55	Ile (ATC) x 5	115	Val (GTG) x 5
57	Ile (ATT) x 5	117	Val (GTT) x 5
59	Leu (CTA) x 5	119	control

The amplified fragments will be cloned between the *EcoRI* and *KpnI* sites of the mammalian expression vector pCDNA3 containing SV40 ori (Invitrogen) and the CMV promoter.

EXAMPLE 2

Transfection of Cos-1 cells

Cos-1 cells in 6-well plates will be transfected with 2 µg of the above expression constructs using lipofectamine (Gibco). GFP fluorescence will be analyzed 36 hrs after transfection. Synthetic *gfp* mRNA expression of transfected cells will also be tested by reverse transcriptase PCR.

EXAMPLE 3

Confocal microscopy

Transfected CV-1 cells can be examined using a Bio-Rad MRC-600 laser-scanning confocal microscope

equipped with a krypton-argon laser and filter sets suitable for the detection of fluorescein and Texas red dyes (Bio-Rad KlyK2), and a Nikon 603 PlanApo numerical aperture 1.2 water-immersion objective.

5 Dual-channel confocal images and video montages of the transfected cells can be suitably composed using ADOBE PhotoShop.

10 The present invention has been described in terms of particular embodiments found or proposed by the present inventors to comprise preferred modes for the practice of the invention. Those of skill in the art will appreciate that, in light of the present disclosure, numerous modifications and changes may be made in the particular embodiments exemplified without
15 departing from the scope of the invention.

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	165	170	175	
5	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190	
10	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205	
15	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220	
20	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
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	35	40	45	
40	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	50	55	60	
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
	65	70	75	80
45	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85	90	95	
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100	105	110	
50	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125	
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140	
55	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155	160
60	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175	
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190	
65	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205	
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220	
70	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

5 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

10 ctg tac aag tga 732
 Leu Tyr Lys

15 <210> 4
 <211> 243
 <212> PRT
 <213> Artificial Sequence

20 <400> 4
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 1 5 10 15

25 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

30 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

35 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

40 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

45 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

50 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

55 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

60 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

65 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

70 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

75 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

80 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

85 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

90 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

95 Leu Tyr Lys

100 <210> 5
 <211> 732
 <212> DNA
 <213> Artificial Sequence

105 <220>

<223> Description of Artificial Sequence: Ala(GCG)5GFP

<220>

<221> CDS

5 <222> (1)..(732)

<400> 5

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15	gtc cca att ctg gtc gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
20	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
25	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
30	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
35	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
40	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
45	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
50	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
55	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
60	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
65	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
70	atc ggc gac ggc cct gtg ctg ctg cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
75	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
80	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
85	ctg tac aag tga	732
	Leu Tyr Lys	

<210> 6
 <211> 243
 <212> PRT
 <213> Artificial Sequence

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<400> 6
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

15

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

25

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

30

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

35

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

40

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

45

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

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Leu Tyr Lys

55

<210> 7
 <211> 732
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: Ala(GCT)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

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 Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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48

	gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
5	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
10	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
15	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
20	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
25	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
30	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
35	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
40	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
45	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
50	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
55	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
60	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
65	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
70	ctg tac aag tga	732
	Leu Tyr Lys	
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	<211> 243	
	<212> PRT	
	<213> Artificial Sequence	
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	20 25 30	

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 5 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 10 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 15 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 20 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 25 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 30 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 35 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 40 Leu Tyr Lys

 45 <210> 9
 <211> 732
 <212> DNA
 <213> Artificial Sequence

 50 <220>
 <223> Description of Artificial Sequence: Arg(AGA)5GFP

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 <222> (1)..(732)
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 65 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 70 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

5	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	240
10	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	288
15	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	336
20	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	384
25	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	432
30	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	480
35	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	528
40	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
45	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
50	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
55	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
60	ctg tac aag tga Leu Tyr Lys	732
65	<210> 10 <211> 243 <212> PRT <213> Artificial Sequence	
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	85	90	95	
5	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
10	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			
15	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			
20	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			
25	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			
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35	<210> 11 <211> 732 <212> DNA <213> Artificial Sequence			
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50	gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30			
55	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45			
60	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
65	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
70	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			

	100	105	110	
5	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			384
10	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
15	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155			480
20	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
25	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
30	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
35	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
40	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235			720
45	ctg tac aag tga Leu Tyr Lys			732
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70	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
75	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
80	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
85	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
90	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
95	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 5 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 10 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 15 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 20 Leu Tyr Lys
 <210> 13
 <211> 732
 <212> DNA
 25 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Arg(CGA)5GFP
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 <221> CDS
 <222> (1)..(732)
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 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 40 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 55 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 60 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 65 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 70 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480

	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
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	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
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10	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
15	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
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	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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	Leu	Tyr	Lys														
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	<211>	243															
	<212>	PRT															
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Leu Tyr Lys

10 <210> 15
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 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> Description of Artificial Sequence: Arg(CGC)5GFP

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 <222> (1)..(732)

<400> 15

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35 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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40 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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45 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

50 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

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 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

65 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

70 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
5	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
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10	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
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	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
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	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
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60	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
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	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
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	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
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	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
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	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
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	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
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	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
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	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
75	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
80	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
85	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
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ctg tac aag tga
Leu Tyr Lys

732

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20
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

25
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

30
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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35
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

40
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

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 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

55
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

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 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

65
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

70
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

75
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

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 225 230 235 240

85
 Leu Tyr Lys

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

30 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

35 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

50 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

55 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

60 atc ggc gac ggc cct gtg ctg ctg cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

65 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
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210 215 220

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ctg tac aag tga 732
Leu Tyr Lys

<210> 20
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				100					105					110			
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	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120				125					
15	gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
			130				135					140					
20	aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
						150					155					160	
25	aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
					165					170					175		
30	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
35	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
			195				200						205				
40	cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
			210				215					220					
45	ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
						230				235						240	
50	ctg	tac	aag	tga													732
	Leu	Tyr	Lys														
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	<212>	PRT															
	<213>	Artificial Sequence															
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		1				5				10					15		
65	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
70	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35					40					45				
75	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50						55				60					
80	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
		65				70				75						80	
85	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
90	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100						105					110			
95	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	

	115	120	125	
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
5	130	135	140	
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155	160
10	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170		175
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185		190
15	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200		205
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
20	210	215	220	
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235	240
25	Leu Tyr Lys			
	<210> 25			
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	Met Asp Asp Asp Asp Ser Lys Gly Glu Leu Phe Thr Gly Val			
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45	gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt			96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
	20 25 30			
50	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc			144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
	35 40 45			
55	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca			192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	50 55 60			
60	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
	65 70 75 80			
65	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85 90 95			
70	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100 105 110			
	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115 120 125			

	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
5	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
10	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
15	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
20	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
25	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
30	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
35	ctg tac aag tga	732
	Leu Tyr Lys	
	<210> 26	
	<211> 243	
	<212> PRT	
	<213> Artificial Sequence	
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	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
45	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
50	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
55	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
60	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
65	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
70	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 5 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 10 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys
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 <211> 732
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 <223> Description of Artificial Sequence: Asp(GAT)5GFP
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 <400> 27
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 Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
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 35
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 40
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 50
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 55
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 60
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 65
 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 70
 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 528
 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

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atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

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cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

15

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

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ctg tac aag tga 732
 Leu Tyr Lys

25

<210> 28
 <211> 243
 <212> PRT
 <213> Artificial Sequence

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<400> 28
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 1 5 10 15

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

50

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

55

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

60

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

65

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

70

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

Leu Tyr Lys

5 <210> 29
 <211> 732
 <212> DNA
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence: Cys(TGC)5GFP

15 <220>
 <221> CDS
 <222> (1)..(732)

<400> 29

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Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	

	210	215	220	
	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
5	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235	240
	ctg tac aag tga			732
	Leu Tyr Lys			
10	<210> 30			
	<211> 243			
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	<213> Artificial Sequence			
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	20	25	30	
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
	35	40	45	
25	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	50	55	60	
30	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
	65	70	75	80
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85	90	95	
35	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100	105	110	
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125	
40	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140	
45	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155	160
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175	
50	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190	
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205	
55	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220	
60	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235	240
	Leu Tyr Lys			
65	<210> 31			
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<220>
 <221> CDS
 <222> (1)..(732)

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<400> 31

atg tgt tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg 48
 Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

15

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

20

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

25

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

30

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

35

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

40

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

45

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

50

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

55

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

60

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

65

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

70

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

<210> 32

<211> 243
 <212> PRT
 <213> Artificial Sequence

5 <400> 32
 Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

10 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

15 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

20 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

25 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

30 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

35 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

40 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

45 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

50 Leu Tyr Lys

55 <210> 33
 <211> 732
 <212> DNA
 <213> Artificial Sequence

60 <220>
 <223> Description of Artificial Sequence: Gln(CAA)5GFP

 <220>
 <221> CDS
 <222> (1)..(732)

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 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

70 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96

	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
5	tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
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	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
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	Tyr	Val	Gln	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
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	Thr	Arg	Ala	Glu	Val	Lys	Phe	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
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	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
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	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
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	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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 5 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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 15 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
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 145 150 155 160
 25 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 30 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
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 65 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
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 50 55 60

	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
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	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
10	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
15	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
20	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
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30	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
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35	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
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40	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
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	195 200 205	
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	35 40 45	
80	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
85	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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 5 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
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 130 135 140
 10 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 15 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 20 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 20 25 30
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 55 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
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 60 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
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 65 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 70 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

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25	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
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	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro							
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	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc							624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr							
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	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val							
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Leu Tyr Lys

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35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
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40 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
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 85 90 95

50 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

55 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

60 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

65 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

70 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624

	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
5	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	672
	210 215 220	
10	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	720
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	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
30	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
35	65 70 75 80	
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
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40	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
45	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
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	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
55	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
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<212> DNA
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5 <220>
 <223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 20 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 25 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 30 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 35 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 40 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 45 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 50 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 55 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 60 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 65 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 70 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 65 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 70 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
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 225 230 235 240

ctg tac aag tga
Leu Tyr Lys

732

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 <211> 243
 <212> PRT
 <213> Artificial Sequence

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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

20 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

25 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

30 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

35 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

40 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

45 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

50 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

55 Leu Tyr Lys

60 <210> 45
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65 <220>
 <223> Description of Artificial Sequence: Gly(GGG)5GFP

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 <222> (1)..(732)

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	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
10	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
15	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
20	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
25	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
30	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
35	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
40	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
45	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
50	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
55	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
60	atc ggc gac ggc cct gtg ctg ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
65	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
70	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
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	Leu Tyr Lys	
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5	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
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	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
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	65					70					75					80
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	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
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			115					120					125			
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
25		130					135					140				
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	145					150					155					160
30	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165						170					175	
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
35				180					185					190		
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
			195				200						205			
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
40		210					215					220				
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	1				5					10					15	
65	gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt
	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
				20					25					30		
	tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc
70	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
			35					40					45			

74

	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
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	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
				100					105					110			
10	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
15		130				135						140					
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150						155					160	
20	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165						170					175		
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
25	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
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	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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	1				5					10					15		
	gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
55	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
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	tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
60	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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	ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50					55				60						
65	ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70				75						80	
70	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	

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10	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			384
15	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
20	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			480
25	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
30	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
35	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
40	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
45	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			720
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75	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
80	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
85	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
90	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
95	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 5 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 10 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 15 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 20 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 45 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 50 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 60 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 65 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 70 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432

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	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145					150					155					160	
10	aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
					165					170					175		
15	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
20	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
			195				200						205				
25	cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210						215					220					
30	ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225					230					235					240	
35	ctg	tac	aag	tga													732
	Leu	Tyr	Lys														
	<210>	52															
	<211>	243															
	<212>	PRT															
	<213>	Artificial Sequence															
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	1				5					10					15		
45	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
50	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35				40						45				
55	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50					55					60					
60	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
65	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
70	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100						105					110			
75	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
80	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130					135					140					
85	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145					150					155					160	
90	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165						170					175		
95	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	

	180	185	190	
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
5	195	200	205	
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220	
10	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235	240
	Leu Tyr Lys			
15	<210> 53			
	<211> 732			
	<212> DNA			
	<213> Artificial Sequence			
20	<220>			
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	1	5	10	15
	gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt			96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
		20	25	30
35	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc			144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
		35	40	45
40	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca			192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
		50	55	60
45	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
		65	70	75
	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
50		85	90	95
	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
		100	105	110
55	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
		115	120	125
60	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
		130	135	140
65	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
	Lys Leu Glu Tyr Asn Thr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
		145	150	155
	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
70		165	170	175

	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576														
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro															
	180 185 190															
5	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624														
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr															
	195 200 205															
10	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672														
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val															
	210 215 220															
15	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720														
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu															
	225 230 235 240															
	ctg tac aag tga	732														
	Leu Tyr Lys															
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25	<400> 54															
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	1 5 10 15															
30	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe															
	20 25 30															
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr															
	35 40 45															
35	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr															
	50 55 60															
40	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro															
	65 70 75 80															
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly															
	85 90 95															
45	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys															
	100 105 110															
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile															
	115 120 125															
50	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His															
	130 135 140															
55	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp															
	145 150 155 160															
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile															
	165 170 175															
60	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro															
	180 185 190															
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr															
	195 200 205															
65	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val															
	210 215 220															
70	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu															
	225 230 235 240															

Leu Tyr Lys

5	<210> 55 <211> 732 <212> DNA <213> Artificial Sequence	
10	<220> <223> Description of Artificial Sequence: Ile(ATC)5GFP	
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25	gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	
30	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	
35	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
40	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	
45	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	
50	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	
55	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	
60	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	
65	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	
70	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	
75	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	
80	atc ggc gac ggc cct gtg ctg ctc cca gac aac cat tac ctg tcc acc 624 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	
85	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

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ctg tac aag tga 732
 Leu Tyr Lys

10

<210> 56
 <211> 243
 <212> PRT
 <213> Artificial Sequence

15

<400> 56
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 1 5 10 15

20

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

25

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

30

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

35

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

40

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

45

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

50

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

55

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

60

Leu Tyr Lys

65

<210> 57
 <211> 732
 <212> DNA
 <213> Artificial Sequence

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<220>
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 <221> CDS
 <222> (1)..(732)

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 1 5 10 15

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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

15 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

20 ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

25 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

30 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

35 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

40 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

45 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

50 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

55 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

60 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

65 atc ggc gac ggc cct gtg ctg ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

70 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

75 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

80 ctg tac aag tga 732
 Leu Tyr Lys

85 <210> 58
 <211> 243

<212> PRT
<213> Artificial Sequence

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
10 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
15 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
20 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
25 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160
35 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190
40 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220
45 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240
50 Leu Tyr Lys

<210> 59
<211> 732
55 <212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5GFP
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<221> CDS
<222> (1)..(732)

<400> 59
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Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
70 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe

	20	25	30	
5	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser 35 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 45			144
10	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys 50 Phe Ile Cys Thr Thr 55 Gly Lys Leu Pro Val 60 Pro Trp Pro Thr			192
15	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser 70 Tyr Gly Val Gln Cys 75 Phe Ser Arg Tyr Pro 80			240
20	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys 85 Gln His Asp Phe Phe 90 Lys Ser Ala Met Pro 95 Glu Gly			288
25	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln 100 Glu Arg Thr Ile Phe Phe 105 Lys Asp Asp Gly Asn Tyr Lys 110			336
30	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg 115 Ala Glu Val Lys Phe 120 Glu Gly Asp Thr Leu Val Asn Arg Ile 125			384
35	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys 130 Gly Ile Asp Phe 135 Lys Glu Asp Gly Asn Ile Leu Gly His 140			432
40	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn 150 Tyr Asn Ser His Asn 155 Val Tyr Ile Met Ala Asp 160			480
45	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn 165 Gly Ile Lys Val Asn Phe 170 Lys Ile Arg His Asn Ile 175			528
50	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly 180 Ser Val Gln Leu Ala Asp 185 His Tyr Gln Gln Asn Thr Pro 190			576
55	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp 195 Gly Pro Val Leu Leu 200 Pro Asp Asn His Tyr 205 Leu Ser Thr			624
60	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys 210 Asp Pro Asn Glu Lys Arg Asp His Met Val 220			672
65	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val 230 Thr Ala Ala Gly Ile Thr 235 His Gly Met Asp Glu 240			720
70	ctg tac aag tga Leu Tyr Lys			732
	<210> 60 <211> 243 <212> PRT <213> Artificial Sequence			
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	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30			
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			

	35	40	45	
5	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
10	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
15	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
20	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			
25	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			
30	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			
35	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			
40	Leu Tyr Lys			
	<210> 61 <211> 732 <212> DNA			
45	<213> Artificial Sequence			
	<220> <223> Description of Artificial Sequence: Leu(CTC)5GFP			
50	<220> <221> CDS <222> (1)..(732)			
	<400> 61			
55	atg ctc ctc ctc ctc ctc agc aag ggc gag gaa ctg ttc act ggc gtg Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15	48		
60	gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	96		
65	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	144		
	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	192		
70	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240		

	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
5	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
10	tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
				100					105					110			
15	acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
20	gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
			130				135					140					
25	aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
						150					155					160	
30	aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
					165					170					175		
35	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
40	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
			195					200					205				
45	cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
			210				215					220					
50	ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
						230					235					240	
55	ctg	tac	aag	tga													732
	Leu	Tyr	Lys														
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	<211>	243															
	<212>	PRT															
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	1					5				10					15		
65	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
70	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35				40						45				
	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
			50				55					60					
	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
						70					75					80	
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 5 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 10 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 15 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 20 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 25 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys
 30
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 1 5 10 15
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 50 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 55 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 60 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 65 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 70 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
5	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
10	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
15	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
20	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
25	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
30	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
35	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
40	ctg tac aag tga	732
	Leu Tyr Lys	
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	<211> 243	
	<212> PRT	
	<213> Artificial Sequence	
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45	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
50	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
55	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
60	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
65	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
70	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 5 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 10 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 15 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys
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 25 <220>
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 30 <222> (1)..(732)
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 35 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 40 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 45 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 50 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 55 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Lys His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 60 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 65 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 70 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 5 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 10 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 15 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 20 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 ctg tac aag tga 732
 Leu Tyr Lys
 25
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 <211> 243
 <212> PRT
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 35 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 40 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 50 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 55 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 60 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 65 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 70 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

5 Leu Tyr Lys

10 <210> 67
 <211> 732
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>
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 <222> (1)..(732)

20 <400> 67

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25 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

30 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

40 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

45 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

50 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

55 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

60 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

65 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

70 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

	195	200	205	
5	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
10	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			720
	ctg tac aag tga Leu Tyr Lys			732
15	<210> 68 <211> 243 <212> PRT <213> Artificial Sequence			
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30	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
35	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
40	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
45	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
50	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			
55	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			
60	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			
65	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240 Leu Tyr Lys			
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<220>

<221> CDS

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<400> 69

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60

65

70

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

ctg tac aag tga 732

Leu Tyr Lys

5 <210> 70
 <211> 243
 <212> PRT
 <213> Artificial Sequence

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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 15 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 20 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 25 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 30 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 35 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 40 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 45 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 50 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 55 Leu Tyr Lys

60 <210> 71
 <211> 732
 <212> DNA
 <213> Artificial Sequence

65 <220>
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>
 <221> CDS
 <222> (1)..(732)

70 <400> 71
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	1				5					10					15		
5	gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
10	tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35					40					45				
15	ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50					55					60					
20	ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
25	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
30	tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
				100					105					110			
35	acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
40	gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135						140					
45	aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145				150					155				160		
50	aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165						170					175		
55	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
60	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
			195				200						205				
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	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215						220					
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	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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 5 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 10 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 15 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 20 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 25 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 30 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 35 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 65 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 70 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

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	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
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	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
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	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
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15	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
20	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
25	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
30	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
35	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
40	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
45	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
50	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
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	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
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	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
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	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	

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5	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
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10	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
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	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
		130					135					140				
15	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	145					150					155					160
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
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20	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
				180					185					190		
25	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200						205			
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		210					215					220				
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55	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
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	tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc
	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
			35					40					45			
60	ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca
	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
		50					55					60				
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	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
		65				70				75						80
70	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
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10	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	384
15	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	432
20	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	480
25	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	528
30	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
35	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
40	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
45	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
50	ctg tac aag tga Leu Tyr Lys	732
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70	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	
75	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
80	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	
85	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	
90	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	
95	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	

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	145					150					155					160	
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
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10	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
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15			195					200					205				
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	210						215					220					
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	1					5				10					15		
	gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
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45	tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
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	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
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	tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
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65	acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
70	gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	

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15	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576		
20	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624		
25	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672		
30	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720		
35	ctg tac aag tga Leu Tyr Lys	732		
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55	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45			
60	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
65	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
70	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
75	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
80	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
85	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
90	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			
95	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			
100	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

5 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225 230 235 240

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<210> 79
15 <211> 732
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

35 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

40 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

45 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

55 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

60 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

65 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

70 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576

	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
5	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	624
	195 200 205	
10	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	672
	210 215 220	
15	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	720
	225 230 235 240	
	ctg tac aag tga Leu Tyr Lys	732
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	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
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	85 90 95	
45	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
50	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
55	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
60	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
65	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
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10 <220>
 <223> Description of Artificial Sequence: Pro(CCG)5GFP

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 Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

20 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

25 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

30 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

35 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

40 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Glu His Asp Phe Phe Lys Ser Ala Met Pro Gly
 85 90 95

40 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

45 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

50 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

55 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

55 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

60 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

65 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

70 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

5 ctg tac aag tga 732
 Leu Tyr Lys

10 <210> 82
 <211> 243
 <212> PRT
 <213> Artificial Sequence

15 <400> 82
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 1 5 10 15
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 30 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 35 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 40 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 45 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 50 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 55 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 60 Leu Tyr Lys

65 <210> 83
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 <212> DNA
 <213> Artificial Sequence

70 <220>
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<221> CDS

<222> (1)..(732)

<400> 83

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10	gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
15	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
20	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
25	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
30	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
35	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
40	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
45	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
50	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
55	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
60	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
65	atc ggc gac ggc cct gtg ctg ctg cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
70	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
75	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240	
80	ctg tac aag tga	732
	Leu Tyr Lys	
	<210> 84	
	<211> 243	
	<212> PRT	

<213> Artificial Sequence

<400> 84

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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 10 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 15 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 20 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 25 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 30 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 35 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 40 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 45 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 50 Leu Tyr Lys

<210> 85

<211> 732

<212> DNA

55 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pro(CGA)5GFP

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<220>

<221> CDS

<222> (1)..(732)

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<400> 85

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 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

5	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser 35 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 45 144
10	ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys 50 Phe Ile Cys Thr Thr 55 Gly Lys Leu Pro Val Pro Trp Pro Thr 60 192
15	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80 240
20	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys 85 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 90 95 288
25	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln 100 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 110 336
30	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala 115 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 120 125 384
35	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys 130 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 140 432
40	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160 480
45	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys 165 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 175 528
50	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly 180 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 190 576
55	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp 195 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 205 624
60	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala 210 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 220 672
65	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240 720
70	ctg tac aag tga Leu Tyr Lys 732
	<210> 86 <211> 243 <212> PRT <213> Artificial Sequence
	<400> 86 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30
	Ser Val Ser 35 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 5 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 10 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 15 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 20 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 25 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 30 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 35 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys
 40
 <210> 87
 <211> 732
 <212> DNA
 <213> Artificial Sequence
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 <220>
 <223> Description of Artificial Sequence: Ser(AGC)5GFP
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 <221> CDS
 <222> (1)..(732)
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 <400> 87
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 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1 5 10 15
 60
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 65
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 70
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 70
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

	65		70		75		80	
5	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc							288
	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly		85		90		95	
10	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag							336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys		100		105		110	
15	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc							384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile		115		120		125	
20	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac							432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		130		135		140	
25	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac							480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		145		150		155	160
30	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att							528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		165		170		175	
35	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca							576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		180		185		190	
40	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc							624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		195		200		205	
45	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc							672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		210		215		220	
50	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag							720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		225		230		235	240
55	ctg tac aag tga							732
	Leu Tyr Lys							
60	<210> 88							
	<211> 243							
	<212> PRT							
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	1 5 10 15							
70	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe							
	20 25 30							
75	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr							
	35 40 45							
80	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr							
	50 55 60							
85	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro							
	65 70 75 80							
90	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly							
	85 90 95							
95	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys							

	100	105	110	
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125	
5	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140	
10	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155	160
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175	
15	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190	
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205	
20	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220	
25	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235	240
	Leu Tyr Lys			
30	<210> 89			
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	1 5 10 15			
	gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt			96
	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
	20 25 30			
50	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc			144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
	35 40 45			
55	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca			192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
	50 55 60			
60	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
	65 70 75 80			
	gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
65	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85 90 95			
	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100 105 110			
70	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384

	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
5	gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
			130				135					140					
10	aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
						150					155					160	
15	aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
					165					170					175		
20	gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
25	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Pro	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
			195				200						205				
30	cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
			210				215					220					
35	ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
						230				235						240	
40	ctg	tac	aag	tga													732
	Leu	Tyr	Lys														
45	<210>	90															
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	<212>	PRT															
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55	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
60	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35			40							45				
65	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50				55						60					
70	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80		
75	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85						90					95		
80	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105						110			
85	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
90	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135						140					
95	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145			150					155						160	

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 5 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 10 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 15 Leu Tyr Lys
 20 <210> 91
 <211> 732
 <212> DNA
 <213> Artificial Sequence
 25 <220>
 <223> Description of Artificial Sequence: Ser(TCA)5GFP
 <220>
 <221> CDS
 <222> (1)..(732)
 30 <400> 91
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 1 5 10 15
 35 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30
 40 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 45 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 50 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 55 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 60 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 65 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 70 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

5 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

10 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

15 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

20 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

ctg tac aag tga 732
 Leu Tyr Lys

25 <210> 92
 <211> 243
 <212> PRT
 <213> Artificial Sequence

30 <400> 92
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 1 5 10 15

35 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

40 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

45 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

50 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

55 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

60 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

65 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

70 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240

5 Leu Tyr Lys

10 <210> 93
 <211> 732
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> Description of Artificial Sequence: Ser(TCC)5GFP

20 <220>
 <221> CDS
 <222> (1)..(732)

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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20 25 30

35 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45

40 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60

45 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80

50 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95

55 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110

60 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

65 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140

70 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

75 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

80 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

85 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

	cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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	ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
	225					230					235					240	
10	ctg	tac	aag	tga													732
	Leu	Tyr	Lys														
15	<210>	94															
	<211>	243															
	<212>	PRT															
	<213>	Artificial Sequence															
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	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
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	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35					40					45				
30	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50						55					60					
	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
35	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
40				100					105					110			
	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
			115					120					125				
45	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130						135					140					
	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150						155					160	
50	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
					165					170					175		
	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
55				180					185					190			
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
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<223> Description of Artificial Sequence: Ser (TCG) 5GFP

<220>

$\langle 222 \rangle$ (1) .. (732)

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Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
180 185 190

atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210 215 220

ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	

ctg tac aag tga 732
Leu Tyr Lys

5 <210> 96
 <211> 243
 <212> PRT
 <213> Artificial Sequence

 <400> 96
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 20 25 30
 15 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 20 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65 70 75 80
 25 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 30 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 35 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 40 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 45 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220
 50 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225 230 235 240
 Leu Tyr Lys

 60 <210> 97
 <211> 732
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ser(TCT)5GFP

 65 <220>
 <221> CDS
 <222> (1)..(732)

 70 <400> 97
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 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

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5	gtc cca att ctc	gtg gaa ctg gat	ggc gat gtg aat ggg	cac aaa ttt	96			
	Val Pro Ile Leu	Val Glu Leu Asp	Gly Asp Val Asn	Gly His Lys Phe				
		20	25	30				
10	tct gtc agc gga	gag ggt gaa ggt	gat gcc aca tac	gga aag ctc acc	144			
	Ser Val Ser Gly	Glu Gly Glu Gly	Asp Ala Thr Tyr	Gly Lys Leu Thr				
		35	40	45				
15	ctg aaa ttc atc	tgc acc act gga	aag ctc cct gtg	cca tgg cca aca	192			
	Leu Lys Phe Ile	Cys Thr Thr Gly	Lys Leu Pro Val	Pro Trp Pro Thr				
		50	55	60				
20	ctg gtc act acc	ttc tct tat ggc	gtg cag tgc ttt	tcc aga tac cca	240			
	Leu Val Thr Thr	Phe Ser Tyr Gly	Val Gln Cys Phe	Ser Arg Tyr Pro				
		65	70	75	80			
25	gac cat atg aag	cag cat gac ttt	ttc aag agc gcc	atg ccc gag ggc	288			
	Asp His Met Lys	Gln His Asp Phe	Phe Lys Ser Ala	Met Pro Glu Gly				
		85	90	95				
30	tat gtg cag gag	aga acc atc ttt	ttc aaa gat gac	ggg aac tac aag	336			
	Tyr Val Gln Glu	Arg Thr Ile Phe	Phe Lys Asp Asp	Gly Asn Tyr Lys				
		100	105	110				
35	acc cgc gct gaa	gtc aag ttc gaa	ggt gac acc ctg	gtg aat aga atc	384			
	Thr Arg Ala Glu	Val Lys Phe Glu	Gly Asp Thr Leu	Val Asn Arg Ile				
		115	120	125				
40	gag ctg aag ggc	att gac ttt aag	gag gat gga aac	att ctc ggc cac	432			
	Glu Leu Lys Gly	Ile Asp Phe Lys	Glu Asp Gly Asn	Ile Leu Gly His				
		130	135	140				
45	aag ctg gaa tac	aac tat aac tcc	cac aat gtg tac	atc atg gcc gac	480			
	Lys Leu Glu Tyr	Asn Tyr Asn Ser	His Asn Val Tyr	Ile Met Ala Asp				
		145	150	155	160			
50	aag caa aag aat	ggc atc aag gtc	aac ttc aag atc	aga cac aac att	528			
	Lys Gln Lys Asn	Gly Ile Lys Val	Asn Phe Lys Ile	Arg His Asn Ile				
		165	170	175				
55	gag gat gga tcc	gtg cag ctg gcc	gac cat tat caa	cag aac act cca	576			
	Glu Asp Gly Ser	Val Gln Leu Ala	Asp His Tyr Gln	Gln Asn Thr Pro				
		180	185	190				
60	atc ggc gac ggc	cct gtg ctc ctc	cca gac aac cat	tac ctg tcc acc	624			
	Ile Gly Asp Gly	Pro Val Leu Leu	Pro Asp Asn His	Tyr Leu Ser Thr				
		195	200	205				
65	cag tct gcc ctg	tct aaa gat ccc	aac gaa aag aga	gac cac atg gtc	672			
	Gln Ser Ala Leu	Ser Lys Asp Pro	Asn Glu Lys Arg	Asp His Met Val				
		210	215	220				
70	ctg ctg gag ttt	gtg acc gct gct	ggg atc aca cat	ggc atg gac gag	720			
	Leu Leu Glu Phe	Val Thr Ala Ala	Gly Ile Thr His	Gly Met Asp Glu				
		225	230	235	240			
75	ctg tac aag tga				732			
	Leu Tyr Lys							
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5	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35					40					45				
	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
		50					55					60					
10	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
15					85					90					95		
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100						105					110			
20	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115						120					125				
	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130					135					140					
25	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150						155					160	
	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
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	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
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35	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200						205				
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		210					215					220					
40	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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	Leu	Tyr	Lys														
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	1					5				10					15		
	gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
65	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
				20					25					30			
	tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
			35					40					45				
70	ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192

	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50						55					60					
5	ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65					70					75					80	
10	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
					85					90					95		
15	tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
				100				105						110			
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	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
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	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
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	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
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	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
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45	atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
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	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
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	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe			
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	115 120 125	
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	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
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	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
30	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
35	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
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	35 40 45	
70	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
75	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
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	85 90 95	
85	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
90	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
95	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	

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10	Glu	Asp	Gly	Ser	Val 180	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
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15	Gln 210	Ser	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
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	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
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	Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
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65	gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
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	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
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	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
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15	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
20	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
25	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
30	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
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60	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
65	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	
70	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	
75	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	
80	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	
85	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	
90	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	
95	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	
100	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 5 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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 40 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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 100 105 110
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 130 135 140
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 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

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10	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210 215	220	672
15	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225 230	235	720
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45	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
50	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
55	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
60	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
65	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
70	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
75	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			
80	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			
85	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			
90	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			
95	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			
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 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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30 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
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 85 90 95

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 100 105 110

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 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125

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 130 135 140

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 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160

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 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175

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 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190

65 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205

70 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720

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 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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	Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
	20 25 30	
15	tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
20	ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
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	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
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	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
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35	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
40	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
45	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
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	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
55	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
60	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
65	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
70	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
75	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
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 35 40 45
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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 85 90 95
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
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 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30
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	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
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	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
10	ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
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	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
20	tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	
25	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
	115 120 125	
30	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
	130 135 140	
35	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
	145 150 155 160	
40	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175	
45	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
	Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190	
50	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
	Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205	
55	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
	Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220	
60	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
	Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
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65	ctg tac aag tga	732
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	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	

	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
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	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
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10	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
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	130						135					140					
20	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
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	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
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25	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
				180					185					190			
	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
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30	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210					215					220					
35	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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	100 105 110	
15	acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	384
	115 120 125	
20	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	432
	130 135 140	
25	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	480
	145 150 155 160	
30	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	528
	165 170 175	
35	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	576
	180 185 190	
40	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	624
	195 200 205	
45	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	672
	210 215 220	
50	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	720
	225 230 235 240	
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75	Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
	35 40 45	
80	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
	50 55 60	
85	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
	65 70 75 80	
90	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
	85 90 95	
95	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
	100 105 110	

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 115 120 125
 5 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 130 135 140
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145 150 155 160
 10 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 165 170 175
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 180 185 190
 15 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 195 200 205
 20 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
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 50 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 35 40 45
 55 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50 55 60
 60 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
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 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 85 90 95
 65 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 100 105 110
 70 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

	115	120	125	
5	gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			432
10	aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			480
15	aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175			528
20	gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190			576
25	atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205			624
30	cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220			672
35	ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240			720
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65	Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60			
70	Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80			
75	Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95			
80	Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110			
85	Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125			
90	Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140			
95	Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160			
100	Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			

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	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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80	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
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85	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
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 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 35 acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
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 40 tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag 240
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
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 45 cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 50 acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 55 aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 60 gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 65 tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 70 atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 65 cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct 576
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 70 gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct 624
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

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70

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primer

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primer

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primer

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primer

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primer

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